



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|-----------------|-------------|----------------------|---------------------|------------------|
| 09/601,168 | 07/28/2000 | RICHARD BENAROUS | 935.38812X00 | 8585 |

20457 7590 04/18/2003

ANTONELLI TERRY STOUT AND KRAUS
SUITE 1800
1300 NORTH SEVENTEENTH STREET
ARLINGTON, VA 22209

EXAMINER

SCHNIZER, HOLLY G

| | |
|----------|--------------|
| ART UNIT | PAPER NUMBER |
|----------|--------------|

1653

DATE MAILED: 04/18/2003

12

Please find below and/or attached an Office communication concerning this application or proceeding.

FILE COPY

Application No.

09/601,168

Applicant(s)

BENAROUS ET AL.

Office Action Summary

Examiner

Holly Schnizer

Art Unit

1653

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --
Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 15 January 2003.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1,3,4,6,7 and 22-50 is/are pending in the application.
- 4a) Of the above claim(s) 6,22-30,33-36 and 38-50 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1,3,4,7,31,32 and 37 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 29 January 1999 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.
If approved, corrected drawings are required in reply to this Office action.
- 12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

- 13) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
a) ☒ All b) ☐ Some * c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☒ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
* See the attached detailed Office action for a list of the certified copies not received.
- 14) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).
a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____
- 4) ☐ Interview Summary (PTO-413) Paper No(s). _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: _____

DETAILED ACTION

Status of the Claims

The Amendment filed January 15, 2003 has been entered and considered. Claims 2 and 5 have been cancelled. Therefore, Claims 1, 3-4, 6-7, and 22-50 are pending. Claims 6, 22-26, 27-30, 33-36, and 38-50 are withdrawn from consideration as being drawn to a non-elected invention. Claims 1, 3-4, 7, 31, 32, and 37 will be considered in this Office Action.

Objections/Rejections Withdrawn

Objection to Specification Withdrawn

The objection to the Specification for recitation of amino acid sequences without reference to a sequence identifier is withdrawn in light of the amendment.

Claim Objections Withdrawn

The objection to Claim 1 is withdrawn in light of the amendment.

The objection of Claims 7, 31, and 32 because they encompass polynucleotides encoding peptides devoid of the F box and peptides devoid of WD units and therefore encompass non-elected subject matter is withdrawn in light of the amendment to Claim 7. Correction is required.

Rejections Withdrawn

The rejections of Claims 2 and 5 under 35 U.S.C. 112, second paragraph are withdrawn in light of the cancellation of these claims.

The rejection of Claim 27 under 35 U.S.C. 112, second paragraph is withdrawn in light of the amendment making it a non-elected claim.

The rejection of Claim 37 under 35 U.S.C. 112, second paragraph is withdrawn in light of the amendment.

The rejection of Claims 7, 27, 31, 32, and 37 under 35 U.S.C. 112, first paragraph for lack of enablement is withdrawn in light of the amendment removing limitations relating to fragments from the claims.

The rejections of Claims 7, 31, and 32 are rejected under 35 U.S.C. 102(a) and (b) as being anticipated by Skowrya et al., Bour et al., Rubinfeld et al., and Inoue et al. is withdrawn in light of the amendment. Skowrya et al., Bour et al., Rubinfeld et al. and Inoue et al. do not teach or suggest that the proteins taught therein contain 7 WD units as found in SEQ ID NO:2 of the present invention.

Objections/Rejections

Claim Objections

As stated in the previous Office Action (with reference to original claim 1) the claims should refer to sequence identifiers as "SEQ ID NO:1" as indicated in 37 C.F.R. 1.821(d) rather than as "SEQ ID No. 1" as is presently claimed in Claim 7. Correction is required.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1, 3, 4, 7, 31, 32, and 37 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 is rejected because it is unclear as to whether the claimed protein must only comprise "units having the following positions in SEQ ID NO:2", interpreted to mean that the protein has an F box and 7 WD units, or whether the claimed protein must comprise the sequences having the following positions in SEQ ID NO:2, which would be interpreted to mean that the protein would have to have those identical sequences. Therefore, the metes and bounds of the claim are unclear. Claims 3, 4, 7, 31, 32, and 37 are also rejected since they depend from Claim 1 but do not correct its deficiencies. Clarification is required.

Steps b) and c) of Claim 7 are unclear. First, the claim is drawn to a nucleic acid sequence coding for the h- β TrCP protein consisting of "b) a DNA sequence which hybridizes under strict conditions with the above sequence" (the above sequence is SEQ ID NO:1 which encodes the h- β TrCP protein). This is confusing since a sequence which hybridizes to SEQ ID NO:1 would be complementary to SEQ ID NO:1 and therefore could not encode the h- β TrCP. Second, step c) recites that the DNA

sequence "results from the sequences a) and b) above and codes for the human protein h- β TrCP". However, sequence a) is the sequence of SEQ ID NO:1 and sequence b) is a sequence which hybridizes to SEQ ID NO:1. Thus, sequences a) and b) are complimentary. The claim is unclear as to what type of sequence "results from" two sequences that are complimentary to each other. Third, it is unclear as to what type of sequence "results from the sequence" of b) and codes for the human protein h- β TrCP since these two sequences are complimentary. Claims 31 and 32 are also rejected since they depend from Claim 7 and do not correct its deficiencies. Correction is required.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1, 3, 4, 7, 31, and 32 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicant is referred to the interim guidelines on written Guidelines published January 5, 2001 in the Federal Register, Vol. 66, No. 4, p. 1099-1111 (available at www.uspto.gov) and the Examiner training Materials on Written Description also available at www.uspto.gov.

The addition of Claims 1, 3, and 4 to this rejection is necessitated by amendment:

Claim 1 has been amended to delete the limitation that the protein has the sequence of SEQ ID NO:2 and to add the limitations previously found in Claim 5. Claim 5 was indicated as allowable because it depended from Claim 1 and thus was drawn to a protein having the sequence of SEQ ID NO:2. However, as amended, the claim is no longer limited to the sequence of SEQ ID NO:2 but may have any number of a wide variety of sequences. Claims 3 and 4 depend from Claim 1 and do not further narrow the genus of sequences claimed.

Applicants contend that the amendment to the claims deleting the limitations relating to peptide fragments is sufficient to overcome the rejection. However, the claims are still drawn to a large genus of protein and nucleic acid sequences as discussed below.

The claims, as amended, are considered to be drawn to any protein or nucleic acid sequence that codes for a protein having the activity of interacting with the Vpu protein of HIV-1, the cell protein I κ B, the cell protein β -catenin, or the skp1p protein and having an F-box and seven WD units. The specification discloses a single β -TrCP protein of SEQ ID NO:2 and various modifications of SEQ ID NO:2 wherein a single domain is removed (i.e. SEQ ID NO:2 without an F-box or SEQ ID NO:2 without the first WD domain). The specification and claims do not provide any guidance with respect to the relationship between specific amino acids within the sequence and function. For example, there is no guidance as to what effect changing amino acids within the F-box would have on skp1p binding. The Specification indicates that such changes could affect the binding. For example, page 2 of the Specification states "it is not certain that

the function of the homologous proteins will be totally conserved. Moreover, there are numerous examples which show that there are always significant differences between species" (p. 2, lines 4-6). Thus, the Specification acknowledges that even two highly homologous proteins may not have identical function. However, the Specification does not teach what identifying characteristics of the sequence of the protein of the present invention give it its identifying function. The written description requirement may be satisfied through disclosure of function and minimal structure when there is a well-established correlation between structure and function. In contrast, without such a correlation, the capability to recognize or understand the structure from the mere recitation of function and minimal structure is highly unlikely and is little more than a wish for possession (see Fed. Reg. (2001) Vol. 66(4) p. 1110, Col. 2, citation 49 citing Eli Lilly, 43 USPQ2d at 1406)).

In addition, the specification and claims do not provide any structural or functional characteristics to distinguish a human β -TrCP from that of other species or proteins that have different functions. For example, Hatakeyama et al. (Proc. Natl. Acad. Sci. (1999) 96: 3859-3863), Skowrya et al. (Cell (1997) 91: 209-219) disclose proteins that appear to have the function of the protein of the claimed invention (clm7), that of binding skp1p. The specification does not provide guidance as to whether these proteins of similar function and structure to that of the protein of the present invention are considered modified β -TrCP proteins. Similarly, the specification acknowledges that the previously identified slimb protein and β -TrCP of Xenope are homologs of the protein of the present invention (p.1 lines 19-35). In fact, as shown in Spevak et al.

(Mol. Cell Biol. (1993) 13: 4953-4966), *Xenopus* β -TrCP has an Fbox and seven WD units that are identical to those of SEQ ID NO:2 (as defined in Claim 1) except for a single amino acid difference in the F-box and a single amino acid difference in the second WD unit. However, the specification does not provide any guidance as to what effect changing a single amino acid in the F-box or WD units would have on activity or the effect that modifications outside the F-box and WD units would have on activity. Moreover, the specification does not provide any structural or functional characteristics of a "human" β -TrCP protein so as to distinguish it from homologs from other species.

Therefore, the scope of the claims include innumerable structural variants (nucleic acid sequences that hybridize and proteins of varying sequences that have an Fbox and seven WD domains) and the genus is highly variant because a significant number of structural differences between genus members is permitted. There is no description of mutational sites that exist in nature, and there is no description of how the structure of the specific SEQ ID NO: relates to the function of the protein or disease. Thus, the common attributes of the genus are not described. One of skill in the art would conclude that applicant was not in possession of the claimed genus because a description of only one member of such a large genus is not representative of the variants of the genus and is insufficient to support the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

Art Unit: 1653

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 1, 3, 4, 7, 31, and 32 are rejected under 35 U.S.C. 102(b) as being anticipated by Spevak et al. (Mol. Cell Biol. (1993) 13: 4953-4966).

Spevak et al. disclose a protein that has the units, an F-box and 7 WD domains, as described in present Claim 1. The sequences of the 1st and 3rd –7th WD units of the protein of Spevak et al. are identical to the corresponding sequences in SEQ ID NO:2 (see figure 9, p. 4960 and sequence alignment attached to this Office Action, claimed positions highlighted). The F-Box and 2nd WD unit each have only one amino acid different than the corresponding units of SEQ ID NO:2 (see attached sequence alignment). Thus, the protein of Spevak et al. is considered to comprise the units having the positions in SEQ ID NO:2 described in Claims 1, 3 and 4. The function of a protein (in this case capability of interacting with proteins degradable by proteasome (clm 1), specifically Vpu, I κ B or β -catenin (clm 3) or skp1p (clm 4)) is dependent on its sequence. Two proteins of the same sequence will have the same structure and thus the same function. Thus, since the protein of Spevak et al. has the same sequence and structure as that of the claimed protein, it is an inherent property of the protein described in Spevak et al. that it would have the same function. Thus, claims 1, 3 and 4 are anticipated by Spevak et al.

The DNA sequence encoding the protein disclosed in Spevak et al. is highly homologous to SEQ ID NO:1 (82% local similarity; see sequence alignment attached)

and would hybridize to a polynucleotide having SEQ ID NO:1. Spevak et al. teach that the β TrCP was expressed in cdc20 cells using an expression vector containing the nucleic acid molecule encoding β -TrCP and means for expression, and therefore Spevak et al. meet the limitations of Claims 1, 7, 31, and 32.

It is noted that Claim 1 is unclear as to whether the claimed protein must only comprise "units having the following positions in SEQ ID NO:2", interpreted to mean that the protein has an F box and 7 WD units, or whether the claimed protein must comprise the sequences having the following positions in SEQ ID NO:2, which would be interpreted to mean that the protein would have to have those identical sequences. If the latter is intended then amendment to clarify this intention would overcome the above rejection under 35 U.S.C. 102(b) since the protein of Spevak et al. has a single amino acid difference from that of SEQ ID NO:2 in each of the F-box and 1st WD unit.

Conclusions

No Claims are allowable. A thorough search of the prior art did not reveal any teaching or suggestions of a protein having the sequence of SEQ ID NO:2, a nucleic acid molecule encoding the protein of SEQ ID NO: 2 or a nucleic acid molecule having the sequence of SEQ ID NO:1, or a method of identifying anti-HIV-1 antiviral agents using a protein having the sequence of SEQ ID NO:2.


Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire **THREE MONTHS** from the mailing date of this action. In the event a first reply is filed within **TWO MONTHS** of the mailing date of this final action and the advisory action is not mailed until after the end of the **THREE-MONTH** shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than **SIX MONTHS** from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Holly Schnizer whose telephone number is (703) 305-3722. The examiner can normally be reached on Monday through Wednesday from 8 am to 5:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christopher Low can be reached on (703) 308-2923. The fax phone numbers for the organization where this application or proceeding is assigned are (703) 308-4242 for regular communications and (703) 308-4242 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 308-0196.


Holly Schnizer
April 16, 2003


CHRISTOPHER S. F. LOW
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1800

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2003, 09:55:06 ; Search time 22 Seconds
(without alignments)
2486.386 Million cell updates/sec

Title: US-09-601-168b-2
Perfect score: 3034
Sequence: 1 MPAFAVILQEKALKEFNSE.....PAAQAEPPRSPTTYTISR 569

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|---------------------|
| 1 | 2397 | 85.6 | 518 | 2 B48088 | beta-transducin re |
| 2 | 1635.5 | 53.9 | 701 | 2 T16607 | hypothetical prote |
| 3 | 690 | 22.7 | 506 | 2 T50211 | WD-repeat protein |
| 4 | 590.5 | 19.5 | 605 | 2 T38932 | probable sulfur me |
| 5 | 545 | 18.0 | 640 | 2 S49932 | MER30 protein - ye |
| 6 | 531.5 | 17.5 | 650 | 2 T46660 | sulfur controller |
| 7 | 520 | 17.1 | 579 | 2 T22703 | hypothetical prote |
| 8 | 519.5 | 17.1 | 267 | 2 S62507 | hypothetical trip-a |
| 9 | 455.5 | 15.0 | 1356 | 2 T18521 | beta transducin-11 |
| 10 | 453 | 14.9 | 775 | 2 T45136 | WD repeat protein |
| 11 | 413.5 | 13.6 | 1227 | 2 A18180 | cell division cont |
| 12 | 399 | 13.2 | 779 | 2 S56245 | WD-40 repeat prote |
| 13 | 396.5 | 13.1 | 703 | 2 T43557 | F-box/WD-repeat pr |
| 14 | 378.5 | 12.5 | 1189 | 2 A12453 | WD-repeat protein |
| 15 | 375 | 12.4 | 1747 | 2 A12453 | WD-40 repeat prote |
| 16 | 374 | 12.3 | 1526 | 2 A12453 | WD-repeat prote |
| 17 | 373.5 | 12.3 | 1258 | 2 A12155 | WD-40 repeat prote |
| 18 | 373.5 | 12.3 | 1258 | 2 A12155 | WD-40 repeat prote |
| 19 | 361.5 | 11.9 | 677 | 2 A12155 | WD-40 repeat prote |
| 20 | 358.5 | 11.8 | 409 | 2 A12155 | WD-40 repeat prote |
| 21 | 354 | 11.7 | 409 | 2 A12155 | WD-40 repeat prote |
| 22 | 354 | 11.7 | 410 | 2 A12155 | WD-40 repeat prote |
| 23 | 341 | 11.2 | 515 | 2 A12155 | WD-40 repeat prote |
| 24 | 339.5 | 11.2 | 775 | 2 A12155 | WD-40 repeat prote |
| 25 | 337 | 11.1 | 1146 | 2 A12155 | WD-40 repeat prote |
| 26 | 336 | 11.1 | 1146 | 2 A12155 | WD-40 repeat prote |
| 27 | 334 | 11.0 | 589 | 2 A12155 | WD-40 repeat prote |
| 28 | 333.5 | 11.0 | 1711 | 2 A12155 | WD-40 repeat prote |
| 29 | 332.5 | 11.0 | 317 | 2 A12155 | WD-40 repeat prote |

| | | | | | |
|----|-------|------|------|----------|--------------------|
| 30 | 330 | 10.9 | 333 | 2 G85034 | probable WD-repeat |
| 31 | 330 | 10.5 | 934 | 2 A61889 | WD-40 repeat prote |
| 32 | 318 | 10.5 | 422 | 2 A56640 | CD4 repeat unit-c |
| 33 | 313.5 | 10.3 | 376 | 2 T19266 | hypothetical prote |
| 34 | 312.5 | 10.3 | 714 | 2 S56893 | hypothetical prote |
| 35 | 312 | 10.3 | 786 | 2 A62375 | WD-40 repeat prote |
| 36 | 312 | 10.3 | 876 | 2 T51507 | WD-40 repeat prote |
| 37 | 307.5 | 10.1 | 1693 | 2 A62415 | beta transducin-11 |
| 38 | 306.5 | 10.1 | 598 | 2 A62415 | WD-repeat prote |
| 39 | 306 | 10.1 | 1189 | 2 A62415 | WD-repeat prote |
| 40 | 305 | 10.1 | 704 | 2 T33263 | transcription init |
| 41 | 299.5 | 9.9 | 1194 | 2 T33263 | transcription init |
| 42 | 298 | 9.8 | 265 | 2 A61890 | apoptotic proteina |
| 43 | 297.5 | 9.8 | 357 | 2 A12099 | WD-repeat prote |
| 44 | 297 | 9.8 | 502 | 2 T41148 | WD-40 repeat prote |
| 45 | 296.5 | 9.8 | 304 | 2 A61837 | WD-40 repeat prote |

ALIGNMENTS

RESULT 1

B48088
beta-transducin repeat-containing protein - African clawed frog
N:Alternate names: beta-Trop
C:Species: Xenopus laevis (African clawed frog)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 21-Jul-2000
C:Accession: B48088
R:Spencer, H., Kasper, B.D., Stralowa, C., Castanon, M.J.
Mol. Cell. Biol. 13, 4953-4966, 1993
A:Title: Saccharomyces cerevisiae cdc5 mutants arrested at a late stage in anaphase
A:Reference number: A48088; MUID:3330289; PMID:8393161
A:Accession: B48088
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-518 <SPE>
A:Cross-references: GB:98268; NID:q295542; PIDN:AA02810.1; PID:q295543
C:Superfamily: unassigned WD repeat proteins; WD repeat homology
C:Keywords: duplication
F:431-462/Domain: WD repeat homology <MD1>

| Query Match | Best Local Similarity | Score | DB 2 | Length | 518 |
|---------------------------|-------------------------------------------------------------|--------------------|-------------------------------------|--------|-----|
| Matches 488; Conservative | 91.6% | Pred. No. 1.2e-193 | 7; Mismatches 8; Indels 30; Gaps 1; | | |
| QY 18 | SSREDCNNGEPKRIPEKNSLRQTNSCARCLQNOETVCLASTAKTENCVAKTLAN 77 | | | | |
| DB 13 | ASEREDCNRPDPKRIPEKNSLRQTNSCARCLQNOETVCLASTAKTENCVAKTLAN 77 | | | | |
| QY 78 | GTSSMIVPKOKRLASYEKEKEKELCYKFEQMSDQVEFEHLISOMCHYOHINSYLK 137 | | | | |
| DB 43 | GTSSMIVPKOKRLASYEKEKEKELCYKFEQMSDQVEFEHLISOMCHYOHINSYLK 137 | | | | |
| QY 138 | PMQORDITVLPARGDHTAENTISYDIAKSLCSAEYVCKEYRVSDDGMKILERRAY 162 | | | | |
| DB 103 | PMQORDITVLPARGDHTAENTISYDIAKSLCSAEYVCKEYRVSDDGMKILERRAY 162 | | | | |
| QY 198 | RTDSLWGLAERGMGOYLKPKPDGNAAPNSFYALPKTIQDLETESNWRGRSL 257 | | | | |
| DB 163 | RTDSLWGLAERGMGOYLKPKPDGNAAPNSFYALPKTIQDLETESNWRGRSL 257 | | | | |
| QY 258 | QRTCHSESTSKGYTCIQYDQKIVSGIRNTLKIQDKNTLECKRII 317 | | | | |
| DB 223 | QRTCHSESTSKGYTCIQYDQKIVSGIRNTLKIQDKNTLECKRII 317 | | | | |
| QY 318 | RYTIGSSDSTAVYWDVNTGEMANT 377 | | | | |
| DB 283 | RYTIGSSDSTAVYWDVNTGEMANT 377 | | | | |
| QY 378 | TITTLRRVLGHRANVAVDQKIVSASGRITKVTSTCEVRLAAGKRGICLQ 437 | | | | |
| DB 343 | TITTLRRVLGHRANVAVDQKIVSASGRITKVTSTCEVRLAAGKRGICLQ 437 | | | | |

OY 438 FROLVVSGSSDNTIRLMDIEGACLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 497
 DB 403 YRDLVYVSGSSDNTIRLMDIEGACLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 462
 OY 498 VVALDPPAPAGTICLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 550
 DB 463 VVALDPPAPAGTICLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 515

RESULT 2

T16607

hypothetical protein K10B2.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16607

R:Miller, N.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans, cosmid K10B2.

A:Accession number: Z16545

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-701 <MIL>

A:Cross-references: EMBL:U28730; NID:g860694; PID:g860695; PIDN:AAA6258.1; CESP:K10B2.1

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:K10B2.1

A:Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3

Query Match

Best local similarity 53.9%; Score 1635.5; DB 2; Length 701;

Matches 328; Conservative 57.7%; Pred. No. 8.1e-119;

Matches 328; Conservative 69; Mismatches 116; Indels 55; Gaps 8;

OY 31 RKIIPEKNSIRQTYNSCARCLNCTVCLASTAMKTEVCYAKTKLAN-----GNS 80

DB 2 RRRREKRAKMGKRRARDDGSIQALVCTST-----IERCF--TAVSNPIFFLESTFFSVF 55

OY 81 SMIVPQR-----KISATYERKEKELCVKYEQWSESDQVEFEHLISOMCHYOHGHSINSY 135

DB 56 SFLEPSRNTQIFLSRSFSSEFVL-----KWEHEQDMDKIKYHRLSHVQLGVNDF 110

OY 136 LKPMLOPDTLPARGLDHIAENLSTYDASLSCAELVCKEYTVSDGMKMKLIER 195

DB 111 IRPMLORDTISNLP-----HVELLIFNVSLSKCEVSTSWRCALARGHMKLIER 166

OY 196 MVRTDSLMLGLAERRGMOYL-----FKNRPDGNAPNSFYAL 235

DB 167 NVASDSLMLGLSEKRWMDKFINISRDMASRYRICEKNYDVNIKROKLDLIMHVFYSKL 226

OY 236 YRRIIDDIETESNRCGRHSIQRHCRSETSKGYCLOYDOKIVSGLRNTIKIMDN 295

DB 227 YRRIIDDIETESNRCGRHSIQRHCRSETSKGYCLOYDOKIVSGLRNTIKIMDN 286

OY 296 TLECKRIHGTGVSVCLOYDERVITGSSDSTVRVMDVNTGEMTLIIHCEAVHLRF 355

DB 287 DVSCHSIIISGHGVSVCLOYDNRVLISSGSSDSTVRVMDVNTGEMTLIIHCEAVHLRF 346

OY 356 NNGMWTGSKDRSIAVMDASPTDITLRVLYGHRVAVVVDPPDKIYASAGDRTIKY 415

DB 347 ANGIWYTSKDRSIAVMDVSPDITIRRVLYGHRVAVVVDPPDKIYASAGDRTIKY 406

OY 416 NNTSGEYVTLNGHKGRIACLOYRDLVYVSGSSDNTIRLMDIEGACLRVLGSEHELVRC 475

DB 407 SHDTLEFVTLNGHKGRIACLOYRDLVYVSGSSDNTIRLMDIEGACLRVLGSEHELVRC 466

OY 476 IFPDNRRIYSGAYDCKIKYMDLVAALDPPAPAGTICLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 535

DB 467 IFPDNRRIYSGAYDCKIKYMDLVAALDPPAPAGTICLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 526

OY 536 SHDDTITLWDFLNDPAAAEPPSPSRT 563

DB 527 SHDDTITLWDFLNDPAAAEPPSPSRT 549

RESULT 3

T50211

WD-repeat protein [Imported] - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000

C:Accession: T50211

R:McDougal, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.;

submitted to the EMBL Data Library, January 2000

A:Reference number: Z25046

A:Accession: T50211

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-506 <MCD>

A:Cross-references: EMBL:AL136538; PIDN:CAB66464.1; GSPDB:GN00066; SPDB:SPAC30.05

A:Experimental source: strain 972h(-); cosmid 630

C:Genetics:

A:Gene: SPAC296.01; SPDB:SPAC30.05

A:Map position: 1

A:Introns: 43/1; 74/3

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match

Best local similarity 22.7%; Score 690; DB 2; Length 506;

Matches 163; Conservative 30.4%; Pred. No. 1.3e-45;

Matches 163; Conservative 104; Mismatches 167; Indels 102; Gaps 15;

OY 67 ENCVAK-----TKLNGTSMIVPQKRIASYTEKEKELCVKYEQWSESDQVEFEHLIS 122

DB 8 KNVKSVSDLTSCDSFSTSSPVLNPLS-----HENNRIDIRDLA 50

OY 123 QMCHYOHGHSINSYCARCLNCTVCLASTAMKTEVCYAKTKLAN-----GNS 80

DB 51 SLSEKGVAVVNHRSLSLFTFTEVP-----EVLAVFSTLDDLCCKMKSKMKRL 106

OY 183 TSDGMLMKLI-----ERVVRTDSLMLG-----LAERGMG----- 213

DB 107 LEDPGIMKALYKMGKPFVENVNLNFEAMRTHKFPQPRENFLLKQNTIIGPOTMPLPQ 166

OY 214 QYLFKNRPDGNAPNSFYALYKTIIDITETISSNRCGRHSIQRHCRSETSKGYCLOYDOKIVSGLRNTIKIMDN 295

DB 167 QYLF-----DSNGRPLNWSYLY-----KEHAHLDNMRHGFVSTPNNNSIREPADODF 217

OY 265 -ETSKGYCLOYDOKIVSGLRNTIKIMDNTECKRIITLGHGVSVCLOYDER-VII 321

DB 218 RATLDSVYCVQYDEIWSGSKDRTVSWMDVNSKFLIYKLGHSGVSLCDDFCRRNLV 277

OY 322 TGSSDSIVRVMDVNTGEMTLIIHCEAVHLRFNNGMWTGSKDRSIAVMDASPTDITLRVLYGHRVAVVVDPPDKIYASAGDRTIKY 415

DB 278 SGSSDSTIIMDMONRRPLKVFEGHTDNLGVVSENYIISSHDHTARVRLDATSPAE 337

OY 380 ITRRVLYGHRVAVVVDPPDKIYASAGDRTIKYMNSTGEFVTLNGHKGRIACLOYDOKIVSGLRNTIKIMDN 295

DB 338 ACM-HVLRGHLASVNSVOYSKKTGLIYASDSRLRTKMTDTTGHCHRIHAHORGIAQAQ 396

OY 438 YRDLVYVSGSSDNTIRLMDIEGACLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 535

DB 397 YNGKFIVSGSSDLTIRLEAASSGKLMLMDGHDLLITFAVFNDEKIVSGSDTIVAIW- 455

OY 498 VVALDPPAPAGTICLRVLGSEHEWCAANDKRYSGAYDCKIKYMDL 550

DB 456 -----FNTGEQHCVLHNSRNSRVPLGDFDHRRIIACYHSSILLWNF 497

RESULT 4

T38932

Probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 26-May-2000

C:Accession: T38932

R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z21818

A:Accession: T38932

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

etc. - nucleic search, using sw model

February 21, 2003, 21:18:21 ; Search time 5545 Seconds
(without alignment)

(without alignments)
11289.474 Million cell updates/sec

Title: US-09-601-168B-1

Sequence: 1 tgcgctgctgcgcctgac.....gtttgccagaaaaaaa 2151

Scoring table: IDENTITY_NUC

Searched: 2054640 seqs, 14551402878 residues

1 number of hits satisfying chosen parameters: 4109280

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database

1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_pl:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_in:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rod:*
36: em_hlg_nam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hgo_hum:*
40: em_hgo_mus:*
41: em_hgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | Description |
|--------|-------|-------|--------|----|-------------|
| No. | Score | Match | Length | ID | |
| ----- | | | | | |

| | | | | | |
|----|--------|-------|--------|----|--------------------|
| 1 | 2151 | 100.0 | 2151 | 6 | AX019507 |
| 2 | 2151 | 100.0 | 2151 | 6 | AX057166 |
| 3 | 2151 | 100.0 | 2151 | 9 | AF129530 |
| 4 | 2151 | 100.0 | 2151 | 9 | HSBTRCP |
| 5 | 2030.4 | 94.4 | 2308 | 9 | BC027994 |
| 6 | 1682.2 | 78.2 | 2175 | 10 | AF081887 |
| 7 | 1663.2 | 77.3 | 1818 | 9 | AF101784 |
| 8 | 1630.4 | 75.8 | 2081 | 10 | BC003989 |
| 9 | 1567.2 | 72.9 | 1979 | 10 | AF110396 |
| 10 | 1451.2 | 67.5 | 1712 | 10 | AF009932 |
| 11 | 1442.8 | 67.1 | 1210 | 10 | AF112979 |
| 12 | 1107.8 | 47.3 | 1671 | 5 | XELSTRPC |
| 13 | 883.4 | 41.1 | 2134 | 9 | AB033379 |
| 14 | 883.4 | 41.1 | 2252 | 9 | AB033380 |
| 15 | 883.4 | 41.1 | 2274 | 9 | AB033281 |
| 16 | 883.4 | 41.1 | 4230 | 9 | AB014596 |
| 17 | 883.4 | 41.1 | 4395 | 9 | BC026213 |
| 18 | 882.4 | 41.0 | 1553 | 9 | AF176022 |
| 19 | 877.8 | 40.8 | 4030 | 10 | BC034261 |
| 20 | 853.2 | 39.7 | 1370 | 10 | AY036079 |
| 21 | 757.8 | 35.2 | 6708 | 9 | AP000252 |
| 22 | 757.8 | 35.2 | 100000 | 9 | AP000212 |
| 23 | 757.8 | 35.2 | 100000 | 17 | AP000134 |
| 24 | 757.8 | 35.2 | 149298 | 9 | AP000031 |
| 25 | 757.8 | 35.2 | 340000 | 9 | AP001711 |
| 26 | 676.4 | 31.4 | 2534 | 9 | AF118898 |
| 27 | 673.2 | 31.3 | 2154 | 3 | AF032878 |
| 28 | 673.2 | 31.3 | 2367 | 3 | AF222924 |
| 29 | 673.2 | 31.3 | 3532 | 3 | AF222923 |
| 30 | 583.2 | 27.1 | 188524 | 2 | AC112602 |
| 31 | 518.8 | 24.1 | 1561 | 6 | AX057148 |
| 32 | 517.8 | 23.8 | 934 | 5 | XU063921 |
| 33 | 502.6 | 23.4 | 1827 | 5 | XU063922 |
| 34 | 463.6 | 21.6 | 2983 | 10 | BC008552 |
| 35 | 454 | 21.1 | 1443 | 3 | AF339101 |
| 36 | 453.2 | 21.1 | 2700 | 3 | AF275523 |
| 37 | 333.2 | 15.5 | 108503 | 9 | AL627424 |
| 38 | 288 | 13.4 | 173634 | 3 | AC009344 |
| 39 | 288 | 13.4 | 230466 | 3 | AC003733 |
| 40 | 277.2 | 12.9 | 40472 | 2 | AC014085 |
| 41 | 252.8 | 11.8 | 17344 | 3 | XU8730 |
| 42 | 232.8 | 10.8 | 143078 | 9 | AL445463 |
| 43 | 225.4 | 10.5 | 231703 | 9 | AC126454 |
| 44 | 225 | 10.5 | 266 | 10 | F391178609 |
| 45 | 216.2 | 10.1 | 261252 | 2 | AC111315 |
| | | | | | AX019507 Sequence |
| | | | | | AX057166 Sequence |
| | | | | | AF129530 Homo sapi |
| | | | | | Y14153 Homo sapien |
| | | | | | BC027994 Homo sapi |
| | | | | | AF081887 Mus muscu |
| | | | | | AF101784 Homo sapi |
| | | | | | BC003989 Mus muscu |
| | | | | | AF110396 Mus muscu |
| | | | | | AF009932 Mus muscu |
| | | | | | AF112979 Mus muscu |
| | | | | | M82656 African cla |
| | | | | | AB033379 Homo sapi |
| | | | | | AB033280 Homo sapi |
| | | | | | AB033281 Homo sapi |
| | | | | | AB014596 Homo sapi |
| | | | | | BC026213 Homo sapi |
| | | | | | AF176022 Homo sapi |
| | | | | | BC034261 Mus muscu |
| | | | | | AY036079 Mus muscu |
| | | | | | AP000252 Homo sapi |
| | | | | | AP000212 Homo sapi |
| | | | | | AP000134 Homo sapi |
| | | | | | AP000031 Homo sapi |
| | | | | | AP001711 Homo sapi |
| | | | | | AF118898 Drosophi |
| | | | | | AF032878 Drosophi |
| | | | | | AF222924 Drosophi |
| | | | | | AF222923 Drosophi |
| | | | | | AC112602 Rattus no |
| | | | | | AX057148 Sequence |
| | | | | | U63921 Xenopus lae |
| | | | | | U63922 Xenopus lae |
| | | | | | BC008552 Mus muscu |
| | | | | | AF339101 Heteroder |
| | | | | | AF275523 Caenorhab |
| | | | | | AL627424 Human DNA |
| </ | | | | | |

ALIGNMENTS

RESULT 1

LOCUS

ACCESSION
VERSION

KEYWORDS
SOURCE

CONCLUSIONS

AUTHORS

TITLE
JOURNAL

linear ~~PAT-07-SEP-2000~~

~~PAT-07-SEP-2000~~

||||| 1141 ACCCTGAGGAGGCTGCGGAGACCGAGCTGCGTCAATGCTTAGACTTTGATGAC 1200
 QY 1270 AAGTACATTTTCTGATGATGAGTATGAACTATTAAGTATGAACAAAGTACTTCT 1329
 Db 1201 AAGTACATGCTTTCTGCTCTGAGATAGACATTAAGTGTGGAACAAAGTACTTCT 1260
 QY 1330 GAATTTGTAAGACCTTAAATGACACAAAGAGGAGTTCCTGTTTGGAGTACAGGAC 1389
 Db 1261 GAATTTGTAAGACCTTAAATGACACAAAGGAGTTCCTGTTTGGAGTACAGGAC 1320
 QY 1390 AGGCTGCTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1449
 Db 1321 AGGCTGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
 QY 1450 GCATGTTTACAGTGTAGTAAAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCT 1509
 Db 1381 GCATGCTGCTGAGTGTGAGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCT 1440
 QY 1570 TTGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 Db 1501 TTGAGACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 QY 1630 AGAGTTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1689
 Db 1561 AGAGTTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
 QY 1690 ATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1749
 Db 1621 ATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
 QY 1750 TCTGAGACATACACCTACATCTCCAGATTA 1779
 Db 1681 TCTGAGACATACACCTACATCTCCAGATTA 1710

RESULT 12
 XELSBTRCP 1671 bp mRNA linear VRT 17-SEP-1993
 LOCUS African clawed frog beta-TrCP mRNA, complete cds.
 DEFINITION M98268
 ACCESSION M98268
 VERSION M98268.1 GI:295542
 KEYWORDS beta-transducin repeats.
 SOURCE Xenopus laevis (library: S. cerevisiae expression library of
 X.laevis oocytes) cDNA to mRNA.
 ORIGIN
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodidae; Xenopus.
 REFERENCE 1 (bases 1 to 1671)
 AUTHORS Spevak, M., Keiper, B. D., Stratowa, C. and Castanon, M. J.
 TITLE Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in
 anaphase are rescued by Xenopus CDNs encoding N-ras or a protein
 with beta-transducin repeats
 JOURNAL Mol. Cell. Biol. 13 (8):4953-4966 (1993)
 MEDLINE 9330289
 PUBMED 8393141

FEATURES
 source
 Location/Qualifiers
 1..1671
 /organism="Xenopus laevis"
 /db_xref="taxon:8155"
 /cell_type="oocyte"
 /tissue_id="S. cerevisiae expression library of X.laevis
 oocytes"
 1..1671
 /gene="beta-TrCP"
 48..1604
 /gene="beta-TrCP"
 /codon_start=1

/protein_id="AA02810.1"
 /db_xref="GI:295543"
 /translation="MESFCSLPPTASEREDCNREPPKITEKNTLRKRLANGT
 SNAIVKORKLSNTEREKELCYKFEQWSECOVEVEHLLSRMKHYGHGINTLYK
 PMLRDFTALPARGLDIAENILSYLADSLCSAEIYKEMRYSDGLMKLIER
 MWRDLSLMLRLARBGWQYLFRNKPDPKPNSEYRALYPIIODIETBSNMG
 RSHLORIHCRSETSKGYCLOYDOKIVSLRNTIKIMDKNLECKRYLMGTSVL
 CLOYDERIVTSSSDSVRYWVNTGEMNTLIHHCDAVLIHLFERNMYTCKRDSI
 AVMDMSATDITLRVILYGRRAVNYVDPEDKITVASGDRITKVNSTICEVRLN
 GHRGIACLOYRRLVYSSSDNTRIMDECGACLRVLEGEHLVRCIRFDRKRV
 GAIDGKIKVMDLVLAALDPRAPAGTILCLRLVESHGRVFLQDEFOIVSSHDTILI
 WDFLNDPGLA"
 1671
 /gene="beta-TrCP"
 BASE COUNT 495 a 341 c 424 g 411 t
 ORIGIN
 Query Match 47.3%; Score 1017.8; DB 5; Length 1671;
 Best Local Similarity 81.8%; Pred. No. 1e-278;
 Matches 1175; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 284 AAACAAACCTGGCAAGGACCTCCAGTATGATGTTGCCAAGCAAGAACTCTGAG 343
 Db 157 AGACAAACCTGGCAAGGACCTCCAGTATGATGTTGCCAAGCAAGAACTCTGAG 216
 QY 344 CAAGCTATGAAAGAAAGAAAGAACTGTGTGCAAAATCTTTGAGCAGTGTGAG 403
 Db 217 CAATTTGCAAGAAAGAAAGAAAGAACTGTGTGCAAAATCTTTGAGCAGTGTGAG 276
 QY 404 ATCAAGTGAATTTGTGGAACATCTTATATCCCAATATGTCTATTACCAATGGGACA 463
 Db 277 ATCAAGTGAATTTGTGGAACATCTTATATCCCAATATGTCTATTACCAATGGGACA 336
 QY 464 TAACTGATATCTTAAACCTATGTTGAGAGAGATTTCAATATGCTCTCCAGCTGGG 523
 Db 337 TAAACACTTACCTTAAACCTATGTTGAGAGAGATTTCAATATGCTCTCCAGCTGGG 396
 QY 524 GATTGATCAATATGCTGAGAACTTCTGTATACCTGATGCAAAATCTATGTGCTG 583
 Db 397 GACTGATCAATATGCTGAGAACTTCTGTATACCTGATGCAAAATCTATGTGCTG 456
 QY 584 CTGAACCTGTGTGCAAGAACTGATGATGATGATGATGATGATGATGATGATGAT 643
 Db 457 CAGAACCTGTGTGCAAGAACTGATGATGATGATGATGATGATGATGATGATGAT 516
 QY 644 TTATCGAGAGAACTGCTGAGAGAGATTTCTGTGAGAGAGCTGGGAGAAAGAGAT 703
 Db 517 TCATAGAGCGGATGCTGAGAGAGATTTCTGTGAGAGAGCTGGGAGAAAGAGAT 576
 QY 704 GGGGACAGTATTTATCAAAACAAACCTCTGAGGAAATGCTCTCCCACTCTTTT 763
 Db 577 GGGGACAGTATTTATCAAAACAAACCTCTGAGGAAATGCTCTCCCACTCTTTT 636
 QY 764 ATAGAGACCTTTATCAAAACAAACCTCTGAGGAAATGCTCTCCCACTCTTTT 823
 Db 637 ACAGAGCGCTTTATCAAAACAAACCTCTGAGGAAATGCTCTCCCACTCTTTT 696
 QY 824 GTGGAAGACATAGTTTACAGAGATTTCACTCCGAGAGTAAACAAAGAGATTACT 883
 Db 697 GTGGAAGACATAGTTTACAGAGATTTCACTCCGAGAGTAAACAAAGAGATTACT 756
 QY 884 GTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 943
 Db 757 GTTACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 816
 QY 944 GGGTAAACAAACATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1003
 Db 817 GGGTAAACAAACATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 876
 QY 1004 GTCTCCAGTATGATGAGAGAGTATATAACAGATGATGATGATGATGATGATGAT 1063
 Db 877 GTCTCCAGTATGATGAGAGAGTATATAACAGATGATGATGATGATGATGATGAT 936

1630 AGAGTTTTCAGTACAGTTGATGATTCAGATTGTCAGTACATGATGACACA 1689
 1561 AGAGTTTTCAGTACAGTTGATGATTCAGATTGTCAGTACATGATGACACA 1620
 1690 ATCTCATCTGGGACTCTCTAATGATCAGCTGCCAAGCAAGCCCGCTCCCT 1749
 1621 ATTCTCATCTGGGACTCTCTAATGATCAGCTGCCAAGCAAGCCCGCTCCCT 1680
 1750 TCTGACATACACTACATCTCCAGATTAAT 1781
 1681 TCTGACATACACTACATCTCCAGATTAAT 1712

RESULT 11
 AF112979 1710 bp mRNA linear ROD 02-MAR-1999
 LOCUS Mus musculus beta-transducin repeat containing protein mRNA,
 DEFINITION complete cds.
 ACCESSION AF112979
 VERSION AF112979.1 GI:4140717
 KEYWORDS

REFERENCE
 AUTHORS Spencer, E., Jiang, J. and Chen, Z. J.
 TITLE Signal-induced ubiquitination of IkappaBalpha by the F-box protein
 JOURNAL Genes Dev. 13 (3), 284-294 (1999)
 MEDLINE 99145465
 PUBMED 9990853
 REFERENCE 2 (bases 1 to 1710)
 AUTHORS Chen, Z. J.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-1998) Molecular Biology and Oncology, UT
 Southwestern Medical Center, 5323 Harry Hines Blvd, Dallas, TX
 75235-9148, USA

FEATURES
 source location/Qualifiers
 1..1710
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 1..1710
 /function="ubiquitinates phosphorylated IkB"
 /note="beta-trcp; F-box protein; IKB-ubiquitin ligase;
 substrate recognition subunit of SCF complex; similar to
 Homo sapiens beta-trcp and Drosophila melanogaster Slimb"
 /codon_start=1
 /product="beta-transducin repeat containing protein"
 /protein_id="AA004181.1"
 /db_xref="GI:4140718"

CDS

BASE COUNT 469 a 399 c 453 g 389 t
 ORIGIN
 Query Match 67.1%; Score 1442.8; DB 10; Length 1710;
 Best Local Similarity 90.2%; Pred. No. 0;
 Matches 1543; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 70 ATGACCCGCGGAGGCGTCTGCAAGAGGCACTAAGTTATGATTCCTCAGAG 129
 1 ATGACCCGCGGAGGCGTCTGCAAGAGGCACTAAGTTATGATTCCTCAGAG 60

QY 130 AGAGAACTGTATATATATGCGAACCCTCAGGAAGTATATACCAAGAAATTCATT 189
 61 AGAGAACTGTATATATATGCGAACCCTCAGGAAGTATATACCAAGAAATTCATT 120
 QY 190 AGACAGCATACAAACAGCTGTGCGAGACTCTGCTTAACCAAGAAACAGATATTAGA 249
 121 AGACAGCATACAAACAGCTGTGCGAGACTCTGCTTAACCAAGAAACAGATATTAGA 180
 QY 250 AGACAGCATACAAACAGCTGTGCGAGACTCTGCTTAACCAAGAAACAGATATTAGA 309
 181 AGACAGCATACAAACAGCTGTGCGAGACTCTGCTTAACCAAGAAACAGATATTAGA 240
 QY 310 AGATGATTTGTCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 369
 241 AGATGATTTGTCGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 300
 QY 370 TGTGTCAATACCTTATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 429
 301 TGTGTCAATACCTTATGAGAGTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAG 360
 QY 430 ATATCCCAATGTGTATACCAACATGCGGCAATTAATCTGATCTTAACTTATG 489
 361 ATATCCCAATGTGTATACCAACATGCGGCAATTAATCTGATCTTAACTTATG 420
 QY 490 CAGAGATTTTCAATACCTGCTGCGAGCTCGGAGATTGATCATATGCTGAGAA 549
 421 CAGAGATTTTCAATACCTGCTGCGAGCTCGGAGATTGATCATATGCTGAGAA 480
 QY 550 CTGTACTACTGAGTCCCAATCACTATGCTGCTGAACTGTGTGCAAGAAATGTTAC 609
 481 CTGTACTACTGAGTCCCAATCACTATGCTGCTGAACTGTGTGCAAGAAATGTTAC 540
 QY 610 CGAGTACCTGTATGAGGCAATGCTGTGGAAGAGCTTATGAGAAATGTTACAGAGAT 669
 541 CGAGTACCTGTATGAGGCAATGCTGTGGAAGAGCTTATGAGAAATGTTACAGAGAT 600
 QY 670 TCTGTGTGAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 601 TCTGTGTGAGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 QY 730 CCTCTGAGGGAATGCTCTCCCACTTTTATAGAGCACTTATCTTAATATATA 789
 661 CCTCTGAGGGAATGCTCTCCCACTTTTATAGAGCACTTATCTTAATATATA 720
 QY 790 CAAGCATTTGAGACATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 849
 721 CAAGCATTTGAGACATTAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 780
 QY 850 CACTGCGAAGTGAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 909
 781 CACTGCGAAGTGAACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 840
 QY 910 GTAAGGCGCTTCCGAGACACACATCAAGTCTGGATTAACCAATGGAATGCAAG 969
 841 GTAAGGCGCTTCCGAGACACACATCAAGTCTGGATTAACCAATGGAATGCAAG 900
 QY 970 GCAATTTCTACAGGCGATACAGGTTCACTGCTGCTCCAGTATGATGAGAGAGTATC 1029
 901 GCAATTTCTACAGGCGATACAGGTTCACTGCTGCTCCAGTATGATGAGAGAGTATC 960
 QY 1030 ATACAGGATATCGGATTCACGCTGAGAGTGTGAGATGATTAACAGGTAATCTTA 1089
 961 ATACAGGATATCGGATTCACGCTGAGAGTGTGAGATGATTAACAGGTAATCTTA 1020
 QY 1090 AACAGGATTCACGCTGAGAGTGTGAGATGATTAACAGGTAATCTTAACAGGATGATG 1149
 1021 AACAGGATTCACGCTGAGAGTGTGAGATGATTAACAGGTAATCTTAACAGGATGATG 1080
 QY 1150 GTGACCTGCTCAAGAGATGCTGCTGATGATGATGATGATGATGATGATGATGAT 1209
 1081 GTGACCTGCTCAAGAGATGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1210 ACCCTCGGAGGCTGCTGCTGAGACACCGAGCTGCTGATGATGATGATGATGATGAT 1269